

SEQUENCE LISTING

<110> Lowery, David E.

Smith, Valdin G.

Kubiak, Teresa M.

Larsen, Martha J.

<120> Drosophila G Protein Coupled Receptors, Nucleic Acids, And Methods Related To
The Same

<130> PHRM0002-103

Earlier Applications

<150> PriorAppNumber : US 10/283,423

<151> PriorFilingDate : 2002-10-30

<150> PriorAppNumber : 09/693,746

<151> PriorFilingDate : 2000-10-20

<150> PriorAppNumber : 09/425,676

<151> PriorFilingDate : 1999-10-22

<160> 187

<170> PatentIn version 3.2

<210> 1

<211> 1803

<212> DNA

<213> D. melanogaster

<400> 1
atggccaaact taagctggct gagcaccatc accaccacct cctcctccat cagcaccaggc 60

cagctgccat tggtcagcac aaccaactgg agcctaacgt cgccggaaac tactagcgct	120
atcttggcg atgtggctgc atcggatgag gataggagcg gcgggatcat tcacaaccag	180
ttcgtgaaa tcttcttcta cgtcctgtac gccacggtct ttgtcctggg tgtcttcgga	240
aatgtcctgg tttgctacgt agttctgagg aatcgggcca tgcagactgt gaccaatata	300
ttcatcacga atctggccct gtcggacata ttgctctgct tcctggcggt gccatttact	360
ccgctttaca cggtcatggg tcgctggcc ttccggcagga gtctgtccca tctgggttcc	420
tttgcccagg gatgcagcat ctacatatcc acgctgaccc tcacccatcgat tgccatcgat	480
cggtacttcg ttatcatata ccccttccat cccgcgtatga agctctccac ctgcateggg	540
atcatagtga gcatctgggt gatagccctg ctggccaccc ttccctacgg catgtacatg	600
aaagatgacca acgagctggt gaacggAACG cagacaggca acgagacccct ggtggaggcc	660
actctaattgc taaacggaag ctttgtggcc cagggatcag gattcatcga ggcgcggac	720
tctacctcgg ccacccaggc ctataatgcag gtgtatgaccc cggtatcaac gggaccggag	780
atgccctatg tgcgggtgta ctgcgaggag aactggccat cgagcagta ccggaaagggtg	840
ttcgggtccca tcacaaccac tctgcagttt gtgtcgccct tcttcatcat ctcgatttgc	900
tacgtgtgaa tatacggtgaa gctaaaccag cggggccaggg ccaagccggg atcgaaatcc	960
tcgagacggg aggaggcgga tcgggatcgc aagaagcgca ccaaccgcat gctcatcgcc	1020
atggtggcg tattcggact cagctggctg cccatcaatg tggtaacat attcgatgac	1080
ttcgtatgaca agtccaacga gtggcgcttc tacatcctat tcttctttgt ggcccactct	1140
attgccatga gctccacctg ctacaatccc ttcctgtacg cctggctgaa cgagaacttc	1200
cgcaaggagt tcaaggcacgt gctccctgc ttaatccct cgaacaacaa catcatcaac	1260
atcaccaggc gctataatcg gagtgatcgg aacacctgtg gtccgcgact gcatcatggc	1320
aaggggatg gtggcatggg cgggtggcagt ctggacggcc acgaccagga cgagaacggc	1380
atcacccagg agacctgtct gccaaaggag aagctgtga ttatccccag ggagccgact	1440
tacggcaatg gcacgggtgc cgtgtcgcca atccttagcg ggcgcggcat taacgcccgc	1500
ctgggtgcacg gtggcgacca tcagatgcac cagctgcagc cgtcacacca tcaacagggt	1560
gagctgacga ggcgaatccg cggcgacca gacgagacgg acggggatta cctggactcc	1620
ggcgacgagc agaccgtgga ggtgcgcttc agcgagacgc cggtcgatcg cacggataat	1680
accaccggga tcagcattct ggagacgagt acgagtcact gccaggactc ggatgtgatg	1740
gtcgagctgg gcgaggcaat cggcgccggt ggtggggcag agctggggag gcgaaatcaac	1800
tga	1803

<210> 2
<211> 600
<212> PRT
<213> D. melanogaster

<400> 2

Met Ala Asn Leu Ser Trp Leu Ser Thr Ile Thr Thr Thr Ser Ser Ser
1 5 10 15

Ile Ser Thr Ser Gln Leu Pro Leu Val Ser Thr Thr Asn Trp Ser Leu
20 25 30

Thr Ser Pro Gly Thr Thr Ser Ala Ile Leu Ala Asp Val Ala Ala Ser
35 40 45

Asp Glu Asp Arg Ser Gly Gly Ile Ile His Asn Gln Phe Val Gln Ile
50 55 60

Phe Phe Tyr Val Leu Tyr Ala Thr Val Phe Val Leu Gly Val Phe Gly
65 70 75 80

Asn Val Leu Val Cys Tyr Val Val Leu Arg Asn Arg Ala Met Gln Thr
85 90 95

Val Thr Asn Ile Phe Ile Thr Asn Leu Ala Leu Ser Asp Ile Leu Leu
100 105 110

Cys Val Leu Ala Val Pro Phe Thr Pro Leu Tyr Thr Phe Met Gly Arg
115 120 125

Trp Ala Phe Gly Arg Ser Leu Cys His Leu Val Ser Phe Ala Gln Gly
130 135 140

Cys Ser Ile Tyr Ile Ser Thr Leu Thr Leu Thr Ser Ile Ala Ile Asp
145 150 155 160

Arg Tyr Phe Val Ile Ile Tyr Pro Phe His Pro Arg Met Lys Leu Ser
165 170 175

Thr Cys Ile Gly Ile Ile Val Ser Ile Trp Val Ile Ala Leu Leu Ala
180 185 190

Thr Val Pro Tyr Gly Met Tyr Met Lys Met Thr Asn Glu Leu Val Asn
195 200 205

Gly Thr Gln Thr Gly Asn Glu Thr Leu Val Glu Ala Thr Leu Met Leu
210 215 220

Asn Gly Ser Phe Val Ala Gln Gly Ser Gly Phe Ile Glu Ala Pro Asp
225 230 235 240

Ser Thr Ser Ala Thr Gln Ala Tyr Met Gln Val Met Thr Ala Gly Ser
245 250 255

Thr Gly Pro Glu Met Pro Tyr Val Arg Val Tyr Cys Glu Glu Asn Trp
260 265 270

Pro Ser Glu Gln Tyr Arg Lys Val Phe Gly Ala Ile Thr Thr Thr Leu
275 280 285

Gln Phe Val Leu Pro Phe Phe Ile Ile Ser Ile Cys Tyr Val Trp Ile
290 295 300

Ser Val Lys Leu Asn Gln Arg Ala Arg Ala Lys Pro Gly Ser Lys Ser
305 310 315 320

Ser Arg Arg Glu Glu Ala Asp Arg Asp Arg Lys Lys Arg Thr Asn Arg
325 330 335

Met Leu Ile Ala Met Val Ala Val Phe Gly Leu Ser Trp Leu Pro Ile
340 345 350

Asn Val Val Asn Ile Phe Asp Asp Phe Asp Asp Lys Ser Asn Glu Trp
355 360 365

Arg Phe Tyr Ile Leu Phe Phe Val Ala His Ser Ile Ala Met Ser
370 375 380

Ser Thr Cys Tyr Asn Pro Phe Leu Tyr Ala Trp Leu Asn Glu Asn Phe
385 390 395 400

Arg Lys Glu Phe Lys His Val Leu Pro Cys Phe Asn Pro Ser Asn Asn
405 410 415

Asn Ile Ile Asn Ile Thr Arg Gly Tyr Asn Arg Ser Asp Arg Asn Thr
420 425 430

Cys Gly Pro Arg Leu His His Gly Lys Gly Asp Gly Gly Met Gly Gly
435 440 445

Gly Ser Leu Asp Ala Asp Asp Gln Asp Glu Asn Gly Ile Thr Gln Glu
450 455 460

Thr Cys Leu Pro Lys Glu Lys Leu Ile Ile Pro Arg Glu Pro Thr
465 470 475 480

Tyr Gly Asn Gly Thr Gly Ala Val Ser Pro Ile Leu Ser Gly Arg Gly
485 490 495

Ile Asn Ala Ala Leu Val His Gly Gly Asp His Gln Met His Gln Leu
500 505 510

Gln Pro Ser His His Gln Gln Val Glu Leu Thr Arg Arg Ile Arg Arg
515 520 525

Arg Thr Asp Glu Thr Asp Gly Asp Tyr Leu Asp Ser Gly Asp Glu Gln
530 535 540

Thr Val Glu Val Arg Phe Ser Glu Thr Pro Phe Val Ser Thr Asp Asn
545 550 555 560

Thr Thr Gly Ile Ser Ile Leu Glu Thr Ser Thr Ser His Cys Gln Asp
565 570 575

Ser Asp Val Met Val Glu Leu Gly Glu Ala Ile Gly Ala Gly Gly
580 585 590

Ala Glu Leu Gly Arg Arg Ile Asn
595 600

<210> 3
<211> 1445
<212> DNA
<213> D. melanogaster

<400> 3
atgaatcaga cggagcccgccagctggca gatggggagc atctgagtggtacggccagc 60
agcagcaaca gcgtgcgcta tctggacgac cggcatccgc tggactacct tgacctggc 120

acgggtgcacg ccctcaaacac cactgccatc aacacacctgg atctgaatga gactgggagc 180
aggccgctgg accccggtgct tatcgatagg ttcctgagca acagggcggt ggacagcccc 240
tggtaccaca tgctcatcag catgtacggc gtgctaattcg tcttcggcgc cctaggcaac 300
accctggttg ttatagccgt catccggaag cccatcatgc gcactgctcg caatctgttc 360
atcctcaacc tggccatatac ggacctactt ttatgcctag tcaccatgcc gctgaccttg 420
atggagatcc tgtccaagta ctggccctac ggctcctgtc ccattcctgtg caaaacgatt 480
gccatgctgc aggcactttg tatttcgtg tcgacaataat ccataacggc cattgccttc 540
gacagatatac aggtgatcgt gtacccacg cgggacagcc tgcagttcgt gggcgcggtg 600
acgatcctgg cggggatctg ggcactggca ctgctgctgg cctcgccgtt gttcgtctac 660
aaggagctga tcaacacacaga cacgcggca ctccctgcagc agatcgccct gcaggacacg 720
atcccgtact gcattgagga ctggccaagt cgcaacgggc gcttctacta ctcgatcttc 780
tcgctgtgcg tacaataacct ggtgcccata ctgatcgctc cggtggcata cttcgggatc 840
tacaacaaggc tgaagagccg catcaccgtg gtggctgtgc agggtcctc cgctcagcgg 900
aagggtggagc gggggcgccg gatgaagcgc accaactgcc tactgatcag catcgccatc 960
atctttggcg tttcttggct gccgctgaac ttttcaacc tgtacgcggc catggagcgc 1020
tcgcccgtca ctcagagcat gctagtccgc tacgccatct gccacatgtat cgccatgagc 1080
tccgcctgtc ccaacccgtt gctctacggc tggctcaacg acaacttccg taaagaattt 1140
caagaactgc totgcccggc ctcagacact aatgttgcgc ttaacggcata cacgacaggc 1200
tgcaacgtcc aggcggcggc ggcgaagcgt cgcaagttgg gcggcgaact ctccaaaggc 1260
gaactcaagc tgctggggcc aggcggcgcc cagagcggta ccggccggcgg ggaaggcggt 1320
ctggcggcca ccgacttcat gaccggccac cacgagggcgc gactgcgcag cgccataacc 1380
gagtcgggtgg ccctcacggc ccacaacccc gtgcctcgg aggtcaccaa gctgatgccg 1440
cggtta 1445

<210> 4

<211> 357

<212> PRT

<213> D. melanogaster

<400> 4

Met Glu Asn Thr Thr Met Leu Ala Asn Ile Ser Leu Asn Ala Thr Arg

1

5

10

15

Asn Glu Glu Asn Ile Thr Ser Phe Phe Thr Asp Glu Glu Trp Leu Ala
20 25 30

Ile Asn Gly Thr Leu Pro Trp Ile Val Gly Phe Phe Phe Gly Val Ile
35 40 45

Ala Ile Thr Gly Phe Phe Gly Asn Leu Leu Val Ile Leu Val Val Val
50 55 60

Phe Asn Asn Asn Met Arg Ser Thr Thr Asn Leu Met Ile Val Asn Leu
65 70 75 80

Ala Ala Ala Asp Leu Met Phe Val Ile Leu Cys Ile Pro Phe Thr Ala
85 90 95

Thr Asp Tyr Met Val Tyr Tyr Trp Pro Tyr Gly Arg Phe Trp Cys Arg
100 105 110

Ser Val Gln Tyr Leu Ile Val Val Thr Ala Phe Ala Ser Ile Tyr Thr
115 120 125

Leu Val Leu Met Ser Ile Asp Arg Phe Leu Ala Val Val His Pro Ile
130 135 140

Arg Ser Arg Met Met Arg Thr Glu Asn Ile Thr Leu Ile Ala Ile Val
145 150 155 160

Thr Leu Trp Ile Val Val Leu Val Val Ser Val Pro Val Ala Phe Thr
165 170 175

His Asp Val Val Val Asp Tyr Asp Ala Lys Lys Asn Ile Thr Tyr Gly
180 185 190

Met Cys Thr Phe Thr Thr Asn Asp Phe Leu Gly Pro Arg Thr Tyr Gln
195 200 205

Val Thr Phe Phe Ile Ser Ser Tyr Leu Leu Pro Leu Met Ile Ile Ser
210 215 220

Gly Leu Tyr Met Arg Met Ile Met Arg Leu Trp Arg Gln Gly Thr Gly
225 230 235 240

Val Arg Met Ser Lys Glu Ser Gln Arg Gly Arg Lys Arg Val Thr Arg
Page 7

245

250

255

Leu Val Val Val Val Val Ile Ala Phe Ala Ser Leu Trp Leu Pro Val
 260 265 270

Gln Leu Ile Leu Leu Lys Ser Leu Asp Val Ile Glu Thr Asn Thr
 275 280 285

Leu Thr Lys Leu Val Ile Gln Val Thr Ala Gln Thr Leu Ala Tyr Ser
 290 295 300

Ser Ser Cys Ile Asn Pro Leu Leu Tyr Ala Phe Leu Ser Glu Asn Phe
 305 310 315 320

Arg Lys Ala Phe Tyr Lys Ala Val Asn Cys Ser Ser Arg Tyr Gln Asn
 325 330 335

Tyr Thr Ser Asp Leu Pro Pro Arg Lys Thr Ser Cys Ala Arg Thr
 340 345 350

Ser Thr Thr Gly Leu
 355

<210> 5

<211> 1376

<212> DNA

<213> D. melanogaster

<400> 5					
atgaatcaga cggagccgc	ccagctggca	gatggggagc	atctgagtgg	atacgccagc	60
agcagcaaca	gcgtgcgcta	tctggacgac	cgcatccgc	tggactacct	tgacctgggc
acggtgacg	ccctcaacac	cactgccatc	aacacctcg	atctgaatga	gactggagc
aggccgctgg	accgggtgct	tatcgatagg	ttcctgagca	acagggcggt	ggacagcccc
tggtaccaca	tgctcatcag	catgtacggc	gtgctaatcg	tcttcggcgc	cctaggcaac
accctggttg	ttatagccgt	catccggaag	cccatcatgc	gcaactgctcg	caatctgttc
atcctaacc	tggccatatac	ggacctactt	ttatgcctag	tcaccatgcc	gctgacccctg
atggagatcc	tgtccaagta	ctggccctac	ggctcctgct	ccatcctgtg	caaaacgatt
gccatgctgc	aggcactttg	tatttcgtg	tcgacaatat	ccataacggc	cattgccttc
					540

gacagatatac aggtgatcgt gtacccacg cgggacagcc tgcagttcgt gggcgcggtg	600
acgatcctgg cggggatctg ggcactggca ctgctgctgg cctcgccgct gttcgtctac	660
aaggagctga tcaacacaga cacgcccggca ctccctgcagc agatcggcct gcaggacacg	720
atcccgtaact gcattgagga ctggccaagt cgcaacgggc gcttctacta ctgcatctc	780
tcgctgtgcg tacaatacct ggtgcccatac ctgatcgtct cggtggcata cttcgggatc	840
tacaacaagc tgaagagccg catcaccgtg gtggctgtgc aggcgtcctc cgctcagcgg	900
aagggtggagc gggggcggcg gatgaagcgc accaactgcc tactgatcag catcgccatc	960
atctttggcg tttcttggct gccgctgaac ttttcaacc tgtacgcggc catggagcgc	1020
tcgcccgtca ctcagagcat gctagtccgc tacgcccatac gccacatgat cggcatgagc	1080
tccgcctgct ccaacccgtt gctctacggc tggctcaacg acaacttccg ctgcaacgtc	1140
caggcggcgg cgccgaagcg tcgcaagttg ggcgccgaac tctccaaagg cgaactcaag	1200
ctgctggggc caggcggcgc ccagagcggt accgcccggc gggaaaggcgg tctggggcc	1260
accgacttca tgaccggcca ccacgaggc ggactgcgcg cgcgcataac cgagtcggtg	1320
gccctcacgg accacaaccc cgtgcctcg gaggtcacca agctgatgcc gcggta	1376

<210> 6

<211> 458

<212> PRT

<213> D. melanogaster

<400> 6

Met Asn Gln Thr Glu Pro Ala Gln Leu Ala Asp Gly Glu His Leu Ser	
1	5
10	15

Gly Tyr Ala Ser Ser Ser Asn Ser Val Arg Tyr Leu Asp Asp Arg His	
20	25
30	

Pro Leu Asp Tyr Leu Asp Leu Gly Thr Val His Ala Leu Asn Thr Thr	
35	40
45	

Ala Ile Asn Thr Ser Asp Leu Asn Glu Thr Gly Ser Arg Pro Leu Asp	
50	55
60	

Pro Val Leu Ile Asp Arg Phe Leu Ser Asn Arg Ala Val Asp Ser Pro	
65	70
75	80

Trp Tyr His Met Leu Ile Ser Met Tyr Gly Val Leu Ile Val Phe Gly
85 90 95

Ala Leu Gly Asn Thr Leu Val Val Ile Ala Val Ile Arg Lys Pro Ile
100 105 110

Met Arg Thr Ala Arg Asn Leu Phe Ile Leu Asn Leu Ala Ile Ser Asp
115 120 125

Leu Leu Leu Cys Leu Val Thr Met Pro Leu Thr Leu Met Glu Ile Leu
130 135 140

Ser Lys Tyr Trp Pro Tyr Gly Ser Cys Ser Ile Leu Cys Lys Thr Ile
145 150 155 160

Ala Met Leu Gln Ala Leu Cys Ile Phe Val Ser Thr Ile Ser Ile Thr
165 170 175

Ala Ile Ala Phe Asp Arg Tyr Gln Val Ile Val Tyr Pro Thr Arg Asp
180 185 190

Ser Leu Gln Phe Val Gly Ala Val Thr Ile Leu Ala Gly Ile Trp Ala
195 200 205

Leu Ala Leu Leu Ala Ser Pro Leu Phe Val Tyr Lys Glu Leu Ile
210 215 220

Asn Thr Asp Thr Pro Ala Leu Leu Gln Gln Ile Gly Leu Gln Asp Thr
225 230 235 240

Ile Pro Tyr Cys Ile Glu Asp Trp Pro Ser Arg Asn Gly Arg Phe Tyr
245 250 255

Tyr Ser Ile Phe Ser Leu Cys Val Gln Tyr Leu Val Pro Ile Leu Ile
260 265 270

Val Ser Val Ala Tyr Phe Gly Ile Tyr Asn Lys Leu Lys Ser Arg Ile
275 280 285

Thr Val Val Ala Val Gln Ala Ser Ser Ala Gln Arg Lys Val Glu Arg
290 295 300

Gly Arg Arg Met Lys Arg Thr Asn Cys Leu Leu Ile Ser Ile Ala Ile
305 310 315 320

Ile Phe Gly Val Ser Trp Leu Pro Leu Asn Phe Phe Asn Leu Tyr Ala
325 330 335

Asp Met Glu Arg Ser Pro Val Thr Gln Ser Met Leu Val Arg Tyr Ala
340 345 350

Ile Cys His Met Ile Gly Met Ser Ser Ala Cys Ser Asn Pro Leu Leu
355 360 365

Tyr Gly Trp Leu Asn Asp Asn Phe Arg Cys Asn Val Gln Ala Ala Ala
370 375 380

Arg Lys Arg Arg Lys Leu Gly Ala Glu Leu Ser Lys Gly Glu Leu Lys
385 390 395 400

Leu Leu Gly Pro Gly Gly Ala Gln Ser Gly Thr Ala Gly Gly Glu Gly
405 410 415

Gly Leu Ala Ala Thr Asp Phe Met Thr Gly His His Glu Gly Gly Leu
420 425 430

Arg Ser Ala Ile Thr Glu Ser Val Ala Leu Thr Asp His Asn Pro Val
435 440 445

Pro Ser Glu Val Thr Lys Leu Met Pro Arg
450 455

<210> 7

<211> 1073

<212> DNA

<213> D. melanogaster

<400> 7
atggagaaca ccacaatgct ggctaatatt agcctaaatg caaccagaaa tgaggagaat 60
atcacctcat tcttcaccga cgaagagtgg ctggccatca atggcacttt gccgtggata 120
gtgggattct tttcggcgt catgccatc acgggattct tcggcaacct gctggtcatc 180
ctgggtgg tttcaacaa caacatgcgc tccaccacca actgtatgtat tgtcaatctg 240
gctgccgctg atctgatgtt cgtaatcctc tgcattccct tcacggccac cgattacatg 300
gtgtactact ggccatatgg aaggttctgg tgccgcagtg tccagtacct gattgtggtg 360

accgccttcg cctccatcta cacgctggtg ctaatgtcca tcgatcggtt cctggcggtg	420
gttcatccca ttcgctcgcg gatgatgagg acggagaaca ttaccctgat tgccatcg	480
actctgtgga tcgtggtgct ggtcgttcg gtgccagtgg cttcaccca cgacgtgg	540
gtggactacg atgcaaagaa gaacatcacc tacggcatgt gcacccac gacgaacgac	600
ttccttggtc cgccaccta ccaggtcacc ttcttcatca gtcctaccc gtcgccc	660
atgatcatca gcggctctcta catgcgcac atcatgcggc tctggcgcc gggAACGGC	720
gtccgcacgt ccaaggagtc gcagcgcggc cgcaagcggg tcacccgact cgtcg	780
gtggtcatcg cttcgccctc gctctggctg cctgtccagc tcatactgct gctcaagtca	840
ctggatgtca tcgagacgaa caccctcacc aagctagtca tccaggtcac cgccca	900
ctggcctaca gcagctcg tataatccg ctgctctacg cttcctctc cgagaattc	960
cggaaggcct tctataaggc cgttaactgc tcctctcgat accagaacta cacatctgat	1020
ttgcccgcgc cgccaaagac gtcctgtgcc aggacctcca ccactggact cta	1073

<210> 8

<211> 357

<212> PRT

<213> D. melanogaster

<400> 8

Met	Glu	Asn	Thr	Thr	Met	Leu	Ala	Asn	Ile	Ser	Leu	Asn	Ala	Thr	Arg
1					5				10				15		

Asn	Glu	Glu	Asn	Ile	Thr	Ser	Phe	Phe	Thr	Asp	Glu	Glu	Trp	Leu	Ala
				20			25				30				

Ile	Asn	Gly	Thr	Leu	Pro	Trp	Ile	Val	Gly	Phe	Phe	Phe	Gly	Val	Ile
						35	40				45				

Ala	Ile	Thr	Gly	Phe	Phe	Gly	Asn	Leu	Leu	Val	Ile	Leu	Val	Val	Val
					50	55				60					

Phe	Asn	Asn	Asn	Met	Arg	Ser	Thr	Asn	Leu	Met	Ile	Val	Asn	Leu
				65	70				75				80	

Ala	Ala	Ala	Asp	Leu	Met	Phe	Val	Ile	Leu	Cys	Ile	Pro	Phe	Thr	Ala
					85			90				95			

Thr Asp Tyr Met Val Tyr Tyr Trp Pro Tyr Gly Arg Phe Trp Cys Arg
100 105 110

Ser Val Gln Tyr Leu Ile Val Val Thr Ala Phe Ala Ser Ile Tyr Thr
115 120 125

Leu Val Leu Met Ser Ile Asp Arg Phe Leu Ala Val Val His Pro Ile
130 135 140

Arg Ser Arg Met Met Arg Thr Glu Asn Ile Thr Leu Ile Ala Ile Val
145 150 155 160

Thr Leu Trp Ile Val Val Leu Val Val Ser Val Pro Val Ala Phe Thr
165 170 175

His Asp Val Val Val Asp Tyr Asp Ala Lys Lys Asn Ile Thr Tyr Gly
180 185 190

Met Cys Thr Phe Thr Thr Asn Asp Phe Leu Gly Pro Arg Thr Tyr Gln
195 200 205

Val Thr Phe Phe Ile Ser Ser Tyr Leu Leu Pro Leu Met Ile Ile Ser
210 215 220

Gly Leu Tyr Met Arg Met Ile Met Arg Leu Trp Arg Gln Gly Thr Gly
225 230 235 240

Val Arg Met Ser Lys Glu Ser Gln Arg Gly Arg Lys Arg Val Thr Arg
245 250 255

Leu Val Val Val Val Val Ile Ala Phe Ala Ser Leu Trp Leu Pro Val
260 265 270

Gln Leu Ile Leu Leu Lys Ser Leu Asp Val Ile Glu Thr Asn Thr
275 280 285

Leu Thr Lys Leu Val Ile Gln Val Thr Ala Gln Thr Leu Ala Tyr Ser
290 295 300

Ser Ser Cys Ile Asn Pro Leu Leu Tyr Ala Phe Leu Ser Glu Asn Phe
305 310 315 320

Arg Lys Ala Phe Tyr Lys Ala Val Asn Cys Ser Ser Arg Tyr Gln Asn
325 330 335

Tyr Thr Ser Asp Leu Pro Pro Pro Arg Lys Thr Ser Cys Ala Arg Thr
340 345 350

Ser Thr Thr Gly Leu
355

<210> 9

<211> 1559

<212> DNA

<213> D. melanogaster

<400> 9
atggagaatc gcagtgactt cgaggcggat gactacggcg acatcagttg gagcaattgg 60
agcaactgga gcaccccccgc cggcgtcctt ttctcgccca tgagcagcgt gctctcgcc 120
agcaaccata cgccccctgcc ggactttggc caggagctcg ccctatccac cagctccctc 180
aatcacagcc agaccctatc caccgaccag cccgcccgtcg gggacgtgga agacgcccggc 240
gaggatgcgg cggcgtccat ggagacgggc tcgtttgcat ttgtggtccc gtggtggcgt 300
caggtgctct ggagcatcct cttcggcggc atggcatttgc tggcgacggg cggttaacctg 360
attgttgcgtct ggatcgtgat gacgaccaag cggatgcggg cggttaaccaa ctatttcata 420
gtgaatctct ccatcgcggg cgcctatggc tccagccctaa acgtcacctt caactactac 480
tatatgctgg atagcgactg gcccttcggc gagttctact gcaagttgtc ccagttcatc 540
gcgatgctaa gcatctgcgc ctcagtgttc accctaattgg ccatctccat cgacagatac 600
gtggccatca tccggccact gcagccgcgg atgagcaagc ggtgcaacct ggcacatcg 660
gcggatctct ggctggcctc cacgctcatc tcctgccccca tggatcatcat ctaccgcacg 720
gaggaggtgc cggccgcgg gctcagcaac cgcacggctc gctacccggg gtggcccgat 780
ggcccccacca atcactccac gatggagtcc ctctacaaca tcctcatcat catyctaacc 840
tacttcctgc ccatcgtctc catgacggtc acctactcgc gctggggcat cgagctctgg 900
ggatccaaga ccatcggcga gtgcacgccc cgccaggtgg araaygtgcg gagtaagcga 960
agggtggta agatgatgat tggatgttc ctgatattcg ccatctgtcg gctgccgttc 1020
cacagctact tcataatcac atcctgctac ccggccatca cggaggcgcctt cttcatccag 1080
gaactctacc tggccatcta ctggctggcc atgagcaact ccatgtacaa tcccattata 1140
tactgctgga tgaattcgcg ctttcgttat ggttcaaga tggtctccg ctggtgccctg 1200

tttgtgcgct tggcactga acccttagt cggcggaga acctgacatc ccgtactcc 1260
tgctccggtt cccggatca caatcgcatc aagcgcaatg ataccagaa atcgatactt 1320
tatacctgtc ccagctcacc caagtgcata cgaattcgc acagcggAAC aggtcgca 1380
gacgctgc ggaacagtct gccggcggag tcactgtcgt ccggcggatc tggtggtgga 1440
ggcacagga aacggttgtc ctaccagcag gaaatgcagc agcgttggtc aggacccaa 1500
agtgccaccc cagtgaccaa ttccagcagt acggccaaca ccacccaaact gctctcctg 1559

<210> 10

<211> 519

<212> PRT

<213> *D. melanogaster*

<400> 10

Met Glu Asn Arg Ser Asp Phe Glu Ala Asp Asp Tyr Gly Asp Ile Ser
1 5 10 15

Trp Ser Asn Trp Ser Asn Trp Ser Thr Pro Ala Gly Val Leu Phe Ser
20 25 30

Ala Met Ser Ser Val Leu Ser Ala Ser Asn His Thr Pro Leu Pro Asp
35 40 45

Phe Gly Gln Glu Leu Ala Leu Ser Thr Ser Ser Phe Asn His Ser Gln
50 55 60

Thr Leu Ser Thr Asp Gln Pro Ala Val Gly Asp Val Glu Asp Ala Ala
65 70 75 80

Glu Asp Ala Ala Ala Ser Met Glu Thr Gly Ser Phe Ala Phe Val Val
85 90 95

Pro Trp Trp Arg Gln Val Leu Trp Ser Ile Leu Phe Gly Gly Met Val
100 105 110

Ile Val Ala Thr Gly Gly Asn Leu Ile Val Val Trp Ile Val Met Thr
115 120 125

Thr Lys Arg Met Arg Thr Val Thr Asn Tyr Phe Ile Val Asn Leu Ser
130 135 140

Ile Ala Asp Ala Met Val Ser Ser Leu Asn Val Thr Phe Asn Tyr Tyr
145 150 155 160

Tyr Met Leu Asp Ser Asp Trp Pro Phe Gly Glu Phe Tyr Cys Lys Leu
165 170 175

Ser Gln Phe Ile Ala Met Leu Ser Ile Cys Ala Ser Val Phe Thr Leu
180 185 190

Met Ala Ile Ser Ile Asp Arg Tyr Val Ala Ile Ile Arg Pro Leu Gln
195 200 205

Pro Arg Met Ser Lys Arg Cys Asn Leu Ala Ile Ala Ala Val Ile Trp
210 215 220

Leu Ala Ser Thr Leu Ile Ser Cys Pro Met Met Ile Ile Tyr Arg Thr
225 230 235 240

Glu Glu Val Pro Val Arg Gly Leu Ser Asn Arg Thr Val Cys Tyr Pro
245 250 255

Glu Trp Pro Asp Gly Pro Thr Asn His Ser Thr Met Glu Ser Leu Tyr
260 265 270

Asn Ile Leu Ile Ile Leu Thr Tyr Phe Leu Pro Ile Val Ser Met
275 280 285

Thr Val Thr Tyr Ser Arg Val Gly Ile Glu Leu Trp Gly Ser Lys Thr
290 295 300

Ile Gly Glu Cys Thr Pro Arg Gln Val Glu Asn Val Arg Ser Lys Arg
305 310 315 320

Arg Val Val Lys Met Met Ile Val Val Leu Ile Phe Ala Ile Cys
325 330 335

Trp Leu Pro Phe His Ser Tyr Phe Ile Ile Thr Ser Cys Tyr Pro Ala
340 345 350

Ile Thr Glu Ala Pro Phe Ile Gln Glu Leu Tyr Leu Ala Ile Tyr Trp
355 360 365

Leu Ala Met Ser Asn Ser Met Tyr Asn Pro Ile Ile Tyr Cys Trp Met
370 375 380

Asn Ser Arg Phe Arg Tyr Gly Phe Lys Met Val Phe Arg Trp Cys Leu
385 390 395 400

Phe Val Arg Val Gly Thr Glu Pro Phe Ser Arg Arg Glu Asn Leu Thr
405 410 415

Ser Arg Tyr Ser Cys Ser Gly Ser Pro Asp His Asn Arg Ile Lys Arg
420 425 430

Asn Asp Thr Gln Lys Ser Ile Leu Tyr Thr Cys Pro Ser Ser Pro Lys
435 440 445

Ser His Arg Ile Ser His Ser Gly Thr Gly Arg Ser Ala Thr Leu Arg
450 455 460

Asn Ser Leu Pro Ala Glu Ser Leu Ser Ser Gly Gly Ser Gly Gly Gly
465 470 475 480

Gly His Arg Lys Arg Leu Ser Tyr Gln Gln Glu Met Gln Gln Arg Trp
485 490 495

Ser Gly Pro Asn Ser Ala Thr Ala Val Thr Asn Ser Ser Ser Thr Ala
500 505 510

Asn Thr Thr Gln Leu Leu Ser
515

<210> 11

<211> 1568

<212> DNA

<213> D. melanogaster

<400> 11
atggagaatc gcagtgactt cgaggcggat gactacggcg acatcagttg gagcaattgg 60
agcaatttggaa gcaactggag caccggcgcc ggcgtccctt tctcggccat gagcagcgtg 120
ctctcgccca gcaaccatac gcctctgccc gactttggcc aggagctcgc cctatccacc 180
agctccctca atcacagccca gaccctatcc accgacctgc ccggcgtcgg ggacgtggaa 240
gacgcccccg aggatgcggc ggcgtccatg gagacgggct cgtttgcatt tgtggtcccc 300
tggtggcgtc aggtgctctg gagcatcctc ttcggcggca tggtcattgt ggcgacggc 360

ggtaaacctga ttgttgtctg gatcgatcg acgaccaagc ggatgcggac ggtaaccaac	420
tatttcatacg taaatctctc catcgccgac gccatgggtgt ccagcctgaa cgtcaccc	480
aactactact acatgctgga tagcgactgg cccttcggcg agttctactg caagttgtcc	540
cagttcatcg cgatgctaag catctgcgcc tcagtgttca ccctaattggc catctccatc	600
gacagatacg tggccatcat ccggccactg cagccgcgg tgagcaagcg gtgcaacctg	660
gccatcgccg cggtcatctg gctggcctcc acgctcatct cctgccccat gatgatcatc	720
taccgcacgg aggaggtgcc ggtccgcggg ctcagcaacc gcacggtctg ctacccggag	780
tggcccgatg ggcccaccaa tcactccacg atggagtccc tctacaacat cctcatcatc	840
attctaacct acttcctgcc catcgctcc atgacggtca cctactcgcg cgtgggcac	900
gagctctggg gatccaagac catcgccgag tgcacgcccc gccaggtggaa gaatgtgcgg	960
agtaagcgaa gggtgtgaa gatgatgatt gtggcgttcc tgatattcgc catctgttgg	1020
ctgccgttcc acagctactt cataatcaca tccctgttacc cggccatcac ggaggcgccc	1080
ttcatccagg aactttacct ggccatctac tggctggcca tgagcaactc catgtacaat	1140
cccattatat actgctggat gaattcgcgc tttcgctatg gttcaagat ggtcttccgc	1200
tggcgcgtt ttgtgcgcgt gggcaactgaa cccttttagtc ggcgggagaa cctgacatcc	1260
cggtaactcct gctccgggttc cccggatcac aatcgcatca agcgcaatga tacccagaaa	1320
tcgataacttt atacctgtcc cagctcaccc aagtcgcac tcgaatttcgcga cagcggaaaca	1380
ggtcgcagtg cgacgctgag gaacagtctg cccggggagt cattgtcgac cgggtggatct	1440
ggaggtggag gacacaggaa acgggtgtcc taccagcagg aaatgcagca gcgggtggta	1500
ggacccaata gtgccaccgc agtgaccaat tccagcagta cggccaaacac cacccaaactg	1560
ctctccctg	1568

<210> 12

<211> 522

<212> PRT

<213> D. melanogaster

<400> 12

Met	Glu	Asn	Arg	Ser	Asp	Phe	Glu	Ala	Asp	Asp	Tyr	Gly	Asp	Ile	Ser
1						5			10					15	

Trp Ser Asn Trp Ser Asn Trp Ser Asn Trp Ser Thr Pro Ala Gly Val

20

25

30

Leu Phe Ser Ala Met Ser Ser Val Leu Ser Ala Ser Asn His Thr Pro
35 40 45

Leu Pro Asp Phe Gly Gln Glu Leu Ala Leu Ser Thr Ser Ser Phe Asn
50 55 60

His Ser Gln Thr Leu Ser Thr Asp Leu Pro Ala Val Gly Asp Val Glu
65 70 75 80

Asp Ala Ala Glu Asp Ala Ala Ser Met Glu Thr Gly Ser Phe Ala
85 90 95

Phe Val Val Pro Trp Trp Arg Gln Val Leu Trp Ser Ile Leu Phe Gly
100 105 110

Gly Met Val Ile Val Ala Thr Gly Gly Asn Leu Ile Val Val Trp Ile
115 120 125

Val Met Thr Thr Lys Arg Met Arg Thr Val Thr Asn Tyr Phe Ile Val
130 135 140

Asn Leu Ser Ile Ala Asp Ala Met Val Ser Ser Leu Asn Val Thr Phe
145 150 155 160

Asn Tyr Tyr Tyr Met Leu Asp Ser Asp Trp Pro Phe Gly Glu Phe Tyr
165 170 175

Cys Lys Leu Ser Gln Phe Ile Ala Met Leu Ser Ile Cys Ala Ser Val
180 185 190

Phe Thr Leu Met Ala Ile Ser Ile Asp Arg Tyr Val Ala Ile Ile Arg
195 200 205

Pro Leu Gln Pro Arg Met Ser Lys Arg Cys Asn Leu Ala Ile Ala Ala
210 215 220

Val Ile Trp Leu Ala Ser Thr Leu Ile Ser Cys Pro Met Met Ile Ile
225 230 235 240

Tyr Arg Thr Glu Glu Val Pro Val Arg Gly Leu Ser Asn Arg Thr Val
245 250 255

Cys Tyr Pro Glu Trp Pro Asp Gly Pro Thr Asn His Ser Thr Met Glu
Page 19

260

265

270

Ser Leu Tyr Asn Ile Leu Ile Ile Leu Thr Tyr Phe Leu Pro Ile
275 280 285

Val Ser Met Thr Val Thr Tyr Ser Arg Val Gly Ile Glu Leu Trp Gly
290 295 300

Ser Lys Thr Ile Gly Glu Cys Thr Pro Arg Gln Val Glu Asn Val Arg
305 310 315 320

Ser Lys Arg Arg Val Val Lys Met Met Ile Val Val Val Leu Ile Phe
325 330 335

Ala Ile Cys Trp Leu Pro Phe His Ser Tyr Phe Ile Ile Thr Ser Cys
340 345 350

Tyr Pro Ala Ile Thr Glu Ala Pro Phe Ile Gln Glu Leu Tyr Leu Ala
355 360 365

Ile Tyr Trp Leu Ala Met Ser Asn Ser Met Tyr Asn Pro Ile Ile Tyr
370 375 380

Cys Trp Met Asn Ser Arg Phe Arg Tyr Gly Phe Lys Met Val Phe Arg
385 390 395 400

Trp Cys Leu Phe Val Arg Val Gly Thr Glu Pro Phe Ser Arg Arg Glu
405 410 415

Asn Leu Thr Ser Arg Tyr Ser Cys Ser Gly Ser Pro Asp His Asn Arg
420 425 430

Ile Lys Arg Asn Asp Thr Gln Lys Ser Ile Leu Tyr Thr Cys Pro Ser
435 440 445

Ser Pro Lys Ser His Arg Ile Ser His Ser Gly Thr Gly Arg Ser Ala
450 455 460

Thr Leu Arg Asn Ser Leu Pro Ala Glu Ser Leu Ser Ser Gly Gly Ser
465 470 475 480

Gly Gly Gly Gly His Arg Lys Arg Leu Ser Tyr Gln Gln Glu Met Gln
485 490 495

Gln Arg Trp Ser Gly Pro Asn Ser Ala Thr Ala Val Thr Asn Ser Ser
Page 20

500

505

510

Ser Thr Ala Asn Thr Thr Gln Leu Leu Ser
515 520

<210> 13

<211> 1394

<212> DNA

<213> D. melanogaster

<400> 13
atggagcacc acaatagcca tctgtgcct ggtggcagcg agaagatgta ctacatacg 60
caccagcagc cgatgctgcg gaacgaggat gataactacc aggagggta cttcatcagg 120
ccggaccctg catccttact ttacaatacc accgcactgc cagcggacga tgaagggtcc 180
aactatggat atggctccac cacaacgctc agtggcctcc agttcgagac ctataatatc 240
actgtgatga tgaactttag ctgtgacgac tatgaccttc tatcggagga catgtggct 300
agtgcctact ttaagatcat cgtctacatg ctctacattc ccatttttat cttcgccctg 360
atcggcaacg gaacggctcg ctatatcg tcattccacac ctcgcacgac cacggtcacc 420
aattactta tagccagctt ggccatcgac gacatcctga tgtccttctt ctgcgttccg 480
tcgtccttca tctcgctgtt catcctgaac tactggcctt ttggcctggc cctctgtcac 540
tttgtgaact actcgcaggc ggtctcagtt ctggtcagcg cctatacttt ggtggcaatt 600
agcattgacc gctacatagc cattatgtgg ccattaaagc cacgcacac aaaacgctat 660
gccacccctca tcacgcggc cgtttggttt attgcacttg ccacccgact tcccataccc 720
atcgtctctg gactcgacat cccaatgtcg ccgtggcaca cggaaatgcga gaaatacatt 780
tgcccgaaaa tgtggccgtc gggacgcag gagtactact acaccctgtc cctctcg 840
ctgcagttcg tcgtgccgtc gggcgtgctc atcttcaccc acgcccggat caccattcg 900
gtctggcga aacgaccggc aggcgaggcg gaaaccaacc gcgaccagcg gatggcacgc 960
tccaaacgga agatggtcaa aatgatgctg acggttgtga ttgtgttcac ctgcgttgg 1020
ctgcccctca atatttgca gctttactg aacgacgagg agttcgccca ctgggatcc 1080
ctgcccgtatg tatggttcg gtttcactgg ctggccatgt cgcaactgctg ctacaatccg 1140
atcatctact gctacatgaa cggccgttcc aggagcggat tcgtccagct gatgcaccgt 1200
atgcccggcc tgcgtcgctg gtgctgcctg cggagcgtcg gtgatcgcat gaacgcaact 1260

tccggAACGG gtcAGCAGTC tcctctcaat cgaatgaaca catccaccac ctacatcagc 1320
gctcgTCGAA agccacgAGC gacatcttg cgagcgaACC cattatcatg cggcgAGACG 1380
tcaccACTGC ggta 1394

<210> 14

<211> 464

<212> PRT

<213> D. melanogaster

<400> 14

Met Glu His His Asn Ser His Leu Leu Pro Gly Gly Ser Glu Lys Met
1 5 10 15

Tyr Tyr Ile Ala His Gln Gln Pro Met Leu Arg Asn Glu Asp Asp Asn
20 25 30

Tyr Gln Glu Gly Tyr Phe Ile Arg Pro Asp Pro Ala Ser Leu Leu Tyr
35 40 45

Asn Thr Thr Ala Leu Pro Ala Asp Asp Glu Gly Ser Asn Tyr Gly Tyr
50 55 60

Gly Ser Thr Thr Thr Leu Ser Gly Leu Gln Phe Glu Thr Tyr Asn Ile
65 70 75 80

Thr Val Met Met Asn Phe Ser Cys Asp Asp Tyr Asp Leu Leu Ser Glu
85 90 95

Asp Met Trp Ser Ser Ala Tyr Phe Lys Ile Ile Val Tyr Met Leu Tyr
100 105 110

Ile Pro Ile Phe Ile Phe Ala Leu Ile Gly Asn Gly Thr Val Cys Tyr
115 120 125

Ile Val Tyr Ser Thr Pro Arg Met Arg Thr Val Thr Asn Tyr Phe Ile
130 135 140

Ala Ser Leu Ala Ile Gly Asp Ile Leu Met Ser Phe Phe Cys Val Pro
145 150 155 160

Ser Ser Phe Ile Ser Leu Phe Ile Leu Asn Tyr Trp Pro Phe Gly Leu

165

170

175

Ala Leu Cys His Phe Val Asn Tyr Ser Gln Ala Val Ser Val Leu Val
180 185 190

Ser Ala Tyr Thr Leu Val Ala Ile Ser Ile Asp Arg Tyr Ile Ala Ile
195 200 205

Met Trp Pro Leu Lys Pro Arg Ile Thr Lys Arg Tyr Ala Thr Phe Ile
210 215 220

Ile Ala Gly Val Trp Phe Ile Ala Leu Ala Thr Ala Leu Pro Ile Pro
225 230 235 240

Ile Val Ser Gly Leu Asp Ile Pro Met Ser Pro Trp His Thr Lys Cys
245 250 255

Glu Lys Tyr Ile Cys Arg Glu Met Trp Pro Ser Arg Thr Gln Glu Tyr
260 265 270

Tyr Tyr Thr Leu Ser Leu Phe Ala Leu Gln Phe Val Val Pro Leu Gly
275 280 285

Val Leu Ile Phe Thr Tyr Ala Arg Ile Thr Ile Arg Val Trp Ala Lys
290 295 300

Arg Pro Pro Gly Glu Ala Glu Thr Asn Arg Asp Gln Arg Met Ala Arg
305 310 315 320

Ser Lys Arg Lys Met Val Lys Met Met Leu Thr Val Val Ile Val Phe
325 330 335

Thr Cys Cys Trp Leu Pro Phe Asn Ile Leu Gln Leu Leu Asn Asp
340 345 350

Glu Glu Phe Ala His Trp Asp Pro Leu Pro Tyr Val Trp Phe Ala Phe
355 360 365

His Trp Leu Ala Met Ser His Cys Cys Tyr Asn Pro Ile Ile Tyr Cys
370 375 380

Tyr Met Asn Ala Arg Phe Arg Ser Gly Phe Val Gln Leu Met His Arg
385 390 395 400

Met Pro Gly Leu Arg Arg Trp Cys Cys Leu Arg Ser Val Gly Asp Arg
Page 23

405

410

415

Met Asn Ala Thr Ser Gly Thr Gly Pro Ala Leu Pro Leu Asn Arg Met
 420 425 430

Asn Thr Ser Thr Thr Tyr Ile Ser Ala Arg Arg Lys Pro Arg Ala Thr
 435 440 445

Ser Leu Arg Ala Asn Pro Leu Ser Cys Gly Glu Thr Ser Pro Leu Arg
 450 455 460

<210> 15

<211> 1556

<212> DNA

<213> D. melanogaster

<400> 15		
atggaggacc acaatagcca tctgttgccct ggtggcagcg agaagatgta ctacatacgct	60	
caccaggcgc cgatgctgctg gaacgaggat gataactacc aggagggtta cttcatcagg	120	
ccggaccctg catccttact ttacaatacc accgcactgc cagcggacga tgaagggtcc	180	
aactatggat atggctccac cacaacgctc agtggcctcc agttcgagac ctataatatc	240	
actgtatga tgaactttag ctgtgacgac tatgacccctc tatcggagga catgtggct	300	
agtgcctact ttaagatcat cgtctacatg ctctacattc ccatctttat cttcgcctg	360	
atcggcaacg gaacggctcg ctatatcgtc tattccacac ctcgcacgac cacggtcacc	420	
aattacttta tagccagctt ggccatcgcc gacatccctga tgccttctt ctgcgttccg	480	
tcgtccttca tctcgctgtt catcctgaac tactggcctt ttggcctggc cctctgtcac	540	
tttgtaact actcgcaggc ggtctcagtt ctggtcagcg cctatacttt ggtggcaatt	600	
agcattgacc gctacatagc cattatgtgg ccattaaagc cacgcacatcac aaaacgctat	660	
gccacccatca tcatcgccgg cgtttggttt attgcacttg ccacccgact tcccataccc	720	
atcgctctg gactcgacat cccaatgtcg ccgtggcaca cggaaatgcga gaaatacatt	780	
tgccgcggaa tgtggccgtc gcgacgcag gacttactt acaccctgtc cctcttcgc	840	
ctgcagttcg tcgtgcccgtc gggcgtgctc atcttaccc acgccccggat caccattcgc	900	
gtctggggcga aacgaccgccc aggcgaggcg gaaaccaacc gcgaccagcg gatggcacgc	960	
tccaaacgga agatggtcaa aatgatgctg acggttgtga ttgtgttac ctgctgtgg	1020	

ctgccccttca atatttgca gcttttactg aacgacgagg agttcgccca ctgggatcct 1080
ctgcccgtatg tgtggttcgc gtttcaactgg ctggccatgt cgcaactgctg ctacaatccg 1140
atcatctact gctacatgaa cgcgcgttgc aggagcggat tcgtccagct gatgcaccgt 1200
atgcccggcc tgcgtcgctg gtgctgcctg cggagcgtcg gtgatcgcat gaacgcaact 1260
tccggtgaga tgactacgaa gtaccatcgc catgtcggcg atgccttatt ccggaaaccc 1320
aaaatatgca ttaggaacgg gtccagcact tcctctcaat cgaatgaaca catccaccac 1380
ctacatcagc gctcgtcgaa agccacgagc gacatcttg cgagcgaacc cattatcatg 1440
cggcgagacg tcaccactgc ggtagctgtc atatcaaaaa ataaaactga ttcaccggtg 1500
cgccgatcgg gaagctcagg tggAACAGAA gcaaACATAA gaAGCACCgA gttttg 1556

<210> 16

<211> 518

<212> PRT

<213> D. melanogaster

<400> 16

Met Glu His His Asn Ser His Leu Leu Pro Gly Gly Ser Glu Lys Met
1 5 10 15

Tyr Tyr Ile Ala His Gln Gln Pro Met Leu Arg Asn Glu Asp Asp Asn
20 25 30

Tyr Gln Glu Gly Tyr Phe Ile Arg Pro Asp Pro Ala Ser Leu Leu Tyr
35 40 45

Asn Thr Thr Ala Leu Pro Ala Asp Asp Glu Gly Ser Asn Tyr Gly Tyr
50 55 60

Gly Ser Thr Thr Thr Leu Ser Gly Leu Gln Phe Glu Thr Tyr Asn Ile
65 70 75 80

Thr Val Met Met Asn Phe Ser Cys Asp Asp Tyr Asp Leu Leu Ser Glu
85 90 95

Asp Met Trp Ser Ser Ala Tyr Phe Lys Ile Ile Val Tyr Met Leu Tyr
100 105 110

Ile Pro Ile Phe Ile Phe Ala Leu Ile Gly Asn Gly Thr Val Cys Tyr
Page 25

115

120

125

Ile Val Tyr Ser Thr Pro Arg Met Arg Thr Val Thr Asn Tyr Phe Ile
130 135 140

Ala Ser Leu Ala Ile Gly Asp Ile Leu Met Ser Phe Phe Cys Val Pro
145 150 155 160

Ser Ser Phe Ile Ser Leu Phe Ile Leu Asn Tyr Trp Pro Phe Gly Leu
165 170 175

Ala Leu Cys His Phe Val Asn Tyr Ser Gln Ala Val Ser Val Leu Val
180 185 190

Ser Ala Tyr Thr Leu Val Ala Ile Ser Ile Asp Arg Tyr Ile Ala Ile
195 200 205

Met Trp Pro Leu Lys Pro Arg Ile Thr Lys Arg Tyr Ala Thr Phe Ile
210 215 220

Ile Ala Gly Val Trp Phe Ile Ala Leu Ala Thr Ala Leu Pro Ile Pro
225 230 235 240

Ile Val Ser Gly Leu Asp Ile Pro Met Ser Pro Trp His Thr Lys Cys
245 250 255

Glu Lys Tyr Ile Cys Arg Glu Met Trp Pro Ser Arg Thr Gln Glu Tyr
260 265 270

Tyr Tyr Thr Leu Ser Leu Phe Ala Leu Gln Phe Val Val Pro Leu Gly
275 280 285

Val Leu Ile Phe Thr Tyr Ala Arg Ile Thr Ile Arg Val Trp Ala Lys
290 295 300

Arg Pro Pro Gly Glu Ala Glu Thr Asn Arg Asp Gln Arg Met Ala Arg
305 310 315 320

Ser Lys Arg Lys Met Val Lys Met Met Leu Thr Val Val Ile Val Phe
325 330 335

Thr Cys Cys Trp Leu Pro Phe Asn Ile Leu Gln Leu Leu Leu Asn Asp
340 345 350

Glu Glu Phe Ala His Trp Asp Pro Leu Pro Tyr Val Trp Phe Ala Phe
Page 26

355

360

365

His Trp Leu Ala Met Ser His Cys Cys Tyr Asn Pro Ile Ile Tyr Cys
370 375 380

Tyr Met Asn Ala Arg Phe Arg Ser Gly Phe Val Gln Leu Met His Arg
385 390 395 400

Met Pro Gly Leu Arg Arg Trp Cys Cys Leu Arg Ser Val Gly Asp Arg
405 410 415

Met Asn Ala Thr Ser Gly Glu Met Thr Thr Lys Tyr His Arg His Val
420 425 430

Gly Asp Ala Leu Phe Arg Lys Pro Lys Ile Cys Ile Arg Asn Gly Ser
435 440 445

Ser Thr Ser Ser Gln Ser Asn Glu His Ile His His Leu His Gln Arg
450 455 460

Ser Ser Lys Ala Thr Ser Asp Ile Phe Ala Ser Glu Pro Ile Ile Met
465 470 475 480

Arg Arg Asp Val Thr Thr Ala Val Ala Val Ile Ser Lys Asn Lys Thr
485 490 495

Asp Ser Pro Val Arg Arg Ser Gly Ser Ser Gly Gly Thr Glu Ala Asn
500 505 510

Ile Arg Ser Thr Glu Phe
515

<210> 17

<211> 1628

<212> DNA

<213> D. melanogaster

<400> 17
atggcaatgg acttaatcga gcaggagtcc cgcctggaat tcctgcccgg agccgaggag 60
gaagcagaat ttgagcgct atacgcggct cccgctgaga ttgtggccct gttgtccatt 120
ttctatgggg gaatcagtat cgtggccgtc attggcaaca ctttggtcat ctgggtggtg 180

gccacgacca ggcaaatgcg gaccgtgaca aatatgtata tcgctaattt ggctttgcc	240
gatgtgatta ttggcctctt ctgcataccca tttcagttcc aggctgcctt gctgcagagt	300
tggAACCTgc cgtggttcat gtgcagcttc tgccccttcg tccaggccct gagtgtaat	360
gtctcggtat tcacgctgac cgccattgca atcgatcggc atagggccat cattaatcca	420
cttagggcac gtcccaccaa gttcgtatcg aagttcataa ttggatgaaat ttggatgctg	480
gccctgctat ttgcggtgcc ctttgcatt gccttcgtg tggaggagtt gaccgaaaga	540
tttcgcgaga acaatgagac ctacaatgtg acgcggccat tctgcatgaa caagaaccta	600
tccgatgatc aattgcaatc ctttcgtac accctggttt ttgtcagta tctgggttcca	660
ttctgtgtca tcagctttgt ctacatccag atggcggtagt gattgtgggg cacacgtgct	720
cctggtaacg cacaggattc acgggacata acgctgtga aaaacaagaa gaaggtcata	780
aaaatgctga ttatcggtt cattatcttt ggactctgct ggctgccact gcagctctat	840
aatattctgt atgtcacgt accggaaatc aacgactacc acttcattag catcgctgg	900
ttttgctgctg atggctggc catgagcaat agctgctaca atccctttat ttatggcatc	960
tacaatgaaa aatttaagcg ggaattcaac aagcgatttgc cggcctgttt ctgcaagttc	1020
aagacgagca tggacgccccca cgaaaggacc tttcgtatgc acacccgcgc cagctccata	1080
aggtaacacct acgccaactc ctcgatgcga atccggagta atctctttgg tccggcgcgt	1140
ggtgtgtca acaatggaa gcccggcttgc catatgccgc gggtgcatgg atccggtgct	1200
aacagcggca ttacaacgg aagttagtggg cagaacaaca atgtcaatgg ccaacatcat	1260
cagcatcaaa gcgtggttac ctttgcggcc actccgggttgc tttcggcacc aggtgttggc	1320
gttgcaatgc cgccgtggcg gcaaaacaac ttcaaacctc tgcattccgaa cgtaatcgaa	1380
tgcgaggacg acgtggcact catggagctg ccatcaacca cgcggccag cgaggagttg	1440
gcattccgggg ccggagtcca gttggccctg ctaagcaggg agagctccag ctgcatttgc	1500
gaacaggaat ttggcagcca aaccgaatgc gatggcacct gcataactcag cgagggtgtcg	1560
cgagtccacc tgccggctc gcaggcgaag gacaaggatg cggcaagtc cttgtggcaa	1620
ccacttta	1628

<210> 18

<211> 542

<212> PRT

<213> D. melanogaster

<400> 18

Met Ala Met Asp Leu Ile Glu Gln Glu Ser Arg Leu Glu Phe Leu Pro
1 5 10 15

Gly Ala Glu Glu Glu Ala Glu Phe Glu Arg Leu Tyr Ala Ala Pro Ala
20 25 30

Glu Ile Val Ala Leu Leu Ser Ile Phe Tyr Gly Gly Ile Ser Ile Val
35 40 45

Ala Val Ile Gly Asn Thr Leu Val Ile Trp Val Val Ala Thr Thr Arg
50 55 60

Gln Met Arg Thr Val Thr Asn Met Tyr Ile Ala Asn Leu Ala Phe Ala
65 70 75 80

Asp Val Ile Ile Gly Leu Phe Cys Ile Pro Phe Gln Phe Gln Ala Ala
85 90 95

Leu Leu Gln Ser Trp Asn Leu Pro Trp Phe Met Cys Ser Phe Cys Pro
100 105 110

Phe Val Gln Ala Leu Ser Val Asn Val Ser Val Phe Thr Leu Thr Ala
115 120 125

Ile Ala Ile Asp Arg His Arg Ala Ile Ile Asn Pro Leu Arg Ala Arg
130 135 140

Pro Thr Lys Phe Val Ser Lys Phe Ile Ile Gly Gly Ile Trp Met Leu
145 150 155 160

Ala Leu Leu Phe Ala Val Pro Phe Ala Ile Ala Phe Arg Val Glu Glu
165 170 175

Leu Thr Glu Arg Phe Arg Glu Asn Asn Glu Thr Tyr Asn Val Thr Arg
180 185 190

Pro Phe Cys Met Asn Lys Asn Leu Ser Asp Asp Gln Leu Gln Ser Phe
195 200 205

Arg Tyr Thr Leu Val Phe Val Gln Tyr Leu Val Pro Phe Cys Val Ile
210 215 220

Ser Phe Val Tyr Ile Gln Met Ala Val Arg Leu Trp Gly Thr Arg Ala

225

230

235

240

Pro Gly Asn Ala Gln Asp Ser Arg Asp Ile Thr Leu Leu Lys Asn Lys
245 250 255

Lys Lys Val Ile Lys Met Leu Ile Ile Val Val Ile Ile Phe Gly Leu
260 265 270

Cys Trp Leu Pro Leu Gln Leu Tyr Asn Ile Leu Tyr Val Thr Ile Pro
275 280 285

Glu Ile Asn Asp Tyr His Phe Ile Ser Ile Val Trp Phe Cys Cys Asp
290 295 300

Trp Leu Ala Met Ser Asn Ser Cys Tyr Asn Pro Phe Ile Tyr Gly Ile
305 310 315 320

Tyr Asn Glu Lys Phe Lys Arg Glu Phe Asn Lys Arg Phe Ala Ala Cys
325 330 335

Phe Cys Lys Phe Lys Thr Ser Met Asp Ala His Glu Arg Thr Phe Ser
340 345 350

Met His Thr Arg Ala Ser Ser Ile Arg Ser Thr Tyr Ala Asn Ser Ser
355 360 365

Met Arg Ile Arg Ser Asn Leu Phe Gly Pro Ala Arg Gly Gly Val Asn
370 375 380

Asn Gly Lys Pro Gly Leu His Met Pro Arg Val His Gly Ser Gly Ala
385 390 395 400

Asn Ser Gly Ile Tyr Asn Gly Ser Ser Gly Gln Asn Asn Asn Val Asn
405 410 415

Gly Gln His His Gln His Gln Ser Val Val Thr Phe Ala Ala Thr Pro
420 425 430

Gly Val Ser Ala Pro Gly Val Gly Val Ala Met Pro Pro Trp Arg Arg
435 440 445

Asn Asn Phe Lys Pro Leu His Pro Asn Val Ile Glu Cys Glu Asp Asp
450 455 460

Val Ala Leu Met Glu Leu Pro Ser Thr Thr Pro Pro Ser Glu Glu Leu
Page 30

465 470 475 480
Ala Ser Gly Ala Gly Val Gln Leu Ala Leu Leu Ser Arg Glu Ser Ser
485 490 495

Ser Cys Ile Cys Glu Gln Glu Phe Gly Ser Gln Thr Glu Cys Asp Gly
500 505 510

Thr Cys Ile Leu Ser Glu Val Ser Arg Val His Leu Pro Gly Ser Gln
515 520 525

Ala Lys Asp Lys Asp Ala Gly Lys Ser Leu Trp Gln Pro Leu
530 535 540

<210> 19
<211> 1451
<212> DNA
<213> D. melanogaster

<400> 19
atgtttacgt ggctgatgtat ggatgtcctc cagtttgta aaggggaaat gacagccgat 60
tcagaggcaa atgcccacaaa ttggtataac acgaacgaga gcttatatac cacggaactg 120
aaccatagat ggatttagtgg tagttccaca attcagccag aggagtcctt ttatggcact 180
gatttgcctt cctatcaaca ttgcatagcc acgcggaatt ctttgctga cttgttca 240
gtggtgctct acggatttgt gtgcattatc ggattatttg gcaacaccct ggtgatctac 300
gtggtgttgc gctttccaa aatgcaaacg gtcacgaata tataatcct gaatctggcg 360
gtggcagacg agtgcttcct gatttgaata ccctttctgc tgtacacaat gcgaatttgc 420
agctggcgat tcggggagtt tatgtcaaa gcctacatgg tgacgcacatc catcacctcc 480
ttcacccgtt cgattttct gctcatcatg tccgcggatc gatataatgc ggtatgccac 540
ccgatttcctt cgccacgata tcgaactctg catattgcca aagtggcttc agcgattgcc 600
tgttcaactt cagcggctt catgtgtccc gtgatccctt atgccagcac tgtggagcag 660
gaggatggca tcaattactc gtgcaacata atgtggccag atgcgtacaa gaagcattcg 720
ggcaccaccc tcaatactgta cacattttc ctaggattcg ccacaccgct gtgctttatc 780
ctgagttctt actacttggt tataaggaaa ctgcgatcgg tgggtcccaa accaggaacg 840
aagtccaagg agaagaggcg ggctcacagg aaggtcactc gactggtaact gacgggtata 900

agtgtataca ttctatgttg gctccctcac tggatttctc aggtggccct gattcactcg 960
 aatcccgccgaaaggacactcctccgactg gaaatactca ttttcctact tctggggca 1020
 ctggtttact cgaattcggc ggtgaatccc atactttatgccttcctaag tgagaacttc 1080
 cggaaagact tcttcaaggc ctttacctgt atgaataagc aggatataaa cgctcaactc 1140
 cagctggagcccaggatgtttt caccacacag ggcagtaaaa agaggggtgg ctccaagcgc 1200
 ctgttgcacca gcaatccgca gattcctcca ctgctgccac tgaatgcggg taacaacaat 1260
 tcatcgacca ccacatcctc gaccacgaca goggaaaaga ccggaaccac ggggacacag 1320
 aaatcatgca attccaatgg caaagtgaca gctccgcccgg agaatttgat tatatgttg 1380
 agcgagcagc aggaggcatt ttgcaccacc gcgagaagag gatcgggcgc agtgcagcag 1440
 acagatttta 1451

<210> 20

<211> 483

<212> PRT

<213> *D. melanogaster*

<400> 20

Met	Phe	Thr	Trp	Leu	Met	Met	Asp	Val	Leu	Gln	Phe	Val	Lys	Gly	Glu
1				5				10							15

Met	Thr	Ala	Asp	Ser	Glu	Ala	Asn	Ala	Thr	Asn	Trp	Tyr	Asn	Thr	Asn
		20					25					30			

Glu	Ser	Leu	Tyr	Thr	Thr	Glu	Leu	Asn	His	Arg	Trp	Ile	Ser	Gly	Ser
		35				40					45				

Ser	Thr	Ile	Gln	Pro	Glu	Glu	Ser	Leu	Tyr	Gly	Thr	Asp	Leu	Pro	Thr
		50			55					60					

Tyr	Gln	His	Cys	Ile	Ala	Thr	Arg	Asn	Ser	Phe	Ala	Asp	Leu	Phe	Thr
65				70					75					80	

Val	Val	Leu	Tyr	Gly	Phe	Val	Cys	Ile	Ile	Gly	Leu	Phe	Gly	Asn	Thr
				85				90					95		

Leu	Val	Ile	Tyr	Val	Val	Leu	Arg	Phe	Ser	Lys	Met	Gln	Thr	Val	Thr
					100			105					110		

Asn Ile Tyr Ile Leu Asn Leu Ala Val Ala Asp Glu Cys Phe Leu Ile
115 120 125

Gly Ile Pro Phe Leu Leu Tyr Thr Met Arg Ile Cys Ser Trp Arg Phe
130 135 140

Gly Glu Phe Met Cys Lys Ala Tyr Met Val Ser Thr Ser Ile Thr Ser
145 150 155 160

Phe Thr Ser Ser Ile Phe Leu Leu Ile Met Ser Ala Asp Arg Tyr Ile
165 170 175

Ala Val Cys His Pro Ile Ser Ser Pro Arg Tyr Arg Thr Leu His Ile
180 185 190

Ala Lys Val Val Ser Ala Ile Ala Trp Ser Thr Ser Ala Val Leu Met
195 200 205

Leu Pro Val Ile Leu Tyr Ala Ser Thr Val Glu Gln Glu Asp Gly Ile
210 215 220

Asn Tyr Ser Cys Asn Ile Met Trp Pro Asp Ala Tyr Lys Lys His Ser
225 230 235 240

Gly Thr Thr Phe Ile Leu Tyr Thr Phe Phe Leu Gly Phe Ala Thr Pro
245 250 255

Leu Cys Phe Ile Leu Ser Phe Tyr Tyr Leu Val Ile Arg Lys Leu Arg
260 265 270

Ser Val Gly Pro Lys Pro Gly Thr Lys Ser Lys Glu Lys Arg Arg Ala
275 280 285

His Arg Lys Val Thr Arg Leu Val Leu Thr Val Ile Ser Val Tyr Ile
290 295 300

Leu Cys Trp Leu Pro His Trp Ile Ser Gln Val Ala Leu Ile His Ser
305 310 315 320

Asn Pro Ala Gln Arg Asp Leu Ser Arg Leu Glu Ile Leu Ile Phe Leu
325 330 335

Leu Leu Gly Ala Leu Val Tyr Ser Asn Ser Ala Val Asn Pro Ile Leu
340 345 350

Tyr Ala Phe Leu Ser Glu Asn Phe Arg Lys Ser Phe Phe Lys Ala Phe
355 360 365

Thr Cys Met Asn Lys Gln Asp Ile Asn Ala Gln Leu Gln Leu Glu Pro
370 375 380

Ser Val Phe Thr Lys Gln Gly Ser Lys Lys Arg Gly Gly Ser Lys Arg
385 390 395 400

Leu Leu Thr Ser Asn Pro Gln Ile Pro Pro Leu Leu Pro Leu Asn Ala
405 410 415

Gly Asn Asn Asn Ser Ser Thr Thr Ser Ser Thr Thr Thr Ala Glu
420 425 430

Lys Thr Gly Thr Thr Gly Thr Gln Lys Ser Cys Asn Ser Asn Gly Lys
435 440 445

Val Thr Ala Pro Pro Glu Asn Leu Ile Ile Cys Leu Ser Glu Gln Gln
450 455 460

Glu Ala Phe Cys Thr Thr Ala Arg Arg Gly Ser Gly Ala Val Gln Gln
465 470 475 480

Thr Asp Leu

<210> 21

<211> 1754

<212> DNA

<213> D. melanogaster

<400> 21
atgttcaact acgaggaggg ggatgccgac caggcggcca tggctgcagc ggctgcctat 60
agggcaactgc tcgactacta tgccaatgcg ccaagtgcgg cgggtcacat agtgcgctc 120
aacgtggcac cctacaatgg aactggaaac ggaggcactg tctccttggc gggcaatgcg 180
acaaggcagct atggcgatga tgataggat ggctatatgg acacccgagcc cagtgacactg 240
gtcaccgaac tggccttctc cctggccacc agttcaagtc caagtcccag ttccacaccc 300
gcttccagct ccagtacttc cactggcatg cccgtctggc tgataccag ctatagcatg 360

attctgctgt tcggcgtgct gggcaacctg ctggtcatct cgacgctggc gcagaatcgc 420
cggatgcgta ccataaccaa cgtgttccctg ctcacacctgg ccatatcgga catgctgctg 480
ggcgtgctct gcatgcccgt caccctggc ggcacccctgc tgcgaaaactt catcttggc 540
gagttcctct gcaagctctt tcagttctcg caagccgcct ccgtggccgt ttcgtcctgg 600
accttggtgg ccatatcctg tgagcgctac tacgcgataat gccatccact gcgctcgcga 660
tcctggcaga caatcagtca cgcctacaag atcatcggt tcatctggct gggcggcatc 720
ctctgcatga cgcccatagc ggtcttttagt caattgatac ccaccagtcg accgggctac 780
tgcaagtgcc gtgagtttg gcccgaccag ggatacggc tcttctacaa catcctgctg 840
gacttcctgc tgctcgtcct gccgcttctc gtcctctgcg tggcctacat cctcatcagc 900
cgtaccctgt acgtaggcat ggccaaggac agcggacgca tcctgcagca atcgctgcct 960
gtttccgcta caacggccgg cggaagcgca ccgaatccgg gcaccagcag cagtagtaac 1020
tgcatcctgg tcctgaccgc caccgcagtc tataatgaaa atagtaacaa taataatgga 1080
aattcagagg gatccgcagg cgaggatca accaatatgg caacgaccac cttgacaacg 1140
agaccaacgg ctccaactgt gatcaccacc accacgacga ccacggtgac gctggccaag 1200
acccctcgc ccagcattcg cgtccacgat gcggcacttc gcaggtccaa cgaggccaag 1260
accctggaga gcaagaagcg tgtggtcaag atgctgttcg tcctggtgct ggagttttc 1320
atctgctgga ctccgctgta cgtgatcaac acgatggtca tgctgatcg accggtggtg 1380
tacgagtatg tcgactacac ggcacatcgt ttcctccagc tgctggccta ctcatccagc 1440
tgctgcaatc cgatcaccta ctgcttcatg aacgcccagct tccggcgcgc ctttgcac 1500
acccccaagg gtctgcctg gctcggtgga gcaggtgcga gcggaggcgt cggtggtgct 1560
gctggtgag gactctccgc cagccaggcg ggccgcaggcc cgggcgccta tgcgagtgcc 1620
aacaccaaca ttagtctcaa tcccgcccta gccatgggtt tgggcacctg gcggagtcgc 1680
tcacgcacac agtttctcaa tgcggtggtg accaccaata gtgcccgcgc cgccgtcaac 1740
agtccctcagc tcta 1754

<210> 22

<211> 584

<212> PRT

<213> D. melanogaster

<400> 22

Met Phe Asn Tyr Glu Glu Gly Asp Ala Asp Gln Ala Ala Met Ala Ala
1 5 10 15

Ala Ala Ala Tyr Arg Ala Leu Leu Asp Tyr Tyr Ala Asn Ala Pro Ser
20 25 30

Ala Ala Gly His Ile Val Ser Leu Asn Val Ala Pro Tyr Asn Gly Thr
35 40 45

Gly Asn Gly Gly Thr Val Ser Leu Ala Gly Asn Ala Thr Ser Ser Tyr
50 55 60

Gly Asp Asp Asp Arg Asp Gly Tyr Met Asp Thr Glu Pro Ser Asp Leu
65 70 75 80

Val Thr Glu Leu Ala Phe Ser Leu Gly Thr Ser Ser Ser Pro Ser Pro
85 90 95

Ser Ser Thr Pro Ala Ser Ser Ser Thr Ser Thr Gly Met Pro Val
100 105 110

Trp Leu Ile Pro Ser Tyr Ser Met Ile Leu Leu Phe Ala Val Leu Gly
115 120 125

Asn Leu Leu Val Ile Ser Thr Leu Val Gln Asn Arg Arg Met Arg Thr
130 135 140

Ile Thr Asn Val Phe Leu Leu Asn Leu Ala Ile Ser Asp Met Leu Leu
145 150 155 160

Gly Val Leu Cys Met Pro Val Thr Leu Val Gly Thr Leu Leu Arg Asn
165 170 175

Phe Ile Phe Gly Glu Phe Leu Cys Lys Leu Phe Gln Phe Ser Gln Ala
180 185 190

Ala Ser Val Ala Val Ser Ser Trp Thr Leu Val Ala Ile Ser Cys Glu
195 200 205

Arg Tyr Tyr Ala Ile Cys His Pro Leu Arg Ser Arg Ser Trp Gln Thr
210 215 220

Ile Ser His Ala Tyr Lys Ile Ile Gly Phe Ile Trp Leu Gly Gly Ile
225 230 235 240

Leu Cys Met Thr Pro Ile Ala Val Phe Ser Gln Leu Ile Pro Thr Ser
245 250 255

Arg Pro Gly Tyr Cys Lys Cys Arg Glu Phe Trp Pro Asp Gln Gly Tyr
260 265 270

Glu Leu Phe Tyr Asn Ile Leu Leu Asp Phe Leu Leu Leu Val Leu Pro
275 280 285

Leu Leu Val Leu Cys Val Ala Tyr Ile Leu Ile Thr Arg Thr Leu Tyr
290 295 300

Val Gly Met Ala Lys Asp Ser Gly Arg Ile Leu Gln Gln Ser Leu Pro
305 310 315 320

Val Ser Ala Thr Thr Ala Gly Gly Ser Ala Pro Asn Pro Gly Thr Ser
325 330 335

Ser Ser Ser Asn Cys Ile Leu Val Leu Thr Ala Thr Ala Val Tyr Asn
340 345 350

Glu Asn Ser Asn Asn Asn Asn Gly Asn Ser Glu Gly Ser Ala Gly Gly
355 360 365

Gly Ser Thr Asn Met Ala Thr Thr Leu Thr Thr Arg Pro Thr Ala
370 375 380

Pro Thr Val Ile Thr Thr Thr Thr Thr Val Thr Leu Ala Lys
385 390 395 400

Thr Ser Ser Pro Ser Ile Arg Val His Asp Ala Ala Leu Arg Arg Ser
405 410 415

Asn Glu Ala Lys Thr Leu Glu Ser Lys Lys Arg Val Val Lys Met Leu
420 425 430

Phe Val Leu Val Leu Glu Phe Phe Ile Cys Trp Thr Pro Leu Tyr Val
435 440 445

Ile Asn Thr Met Val Met Leu Ile Gly Pro Val Val Tyr Glu Tyr Val
450 455 460

Asp Tyr Thr Ala Ile Ser Phe Leu Gln Leu Leu Ala Tyr Ser Ser Ser
465 470 475 480

Cys Cys Asn Pro Ile Thr Tyr Cys Phe Met Asn Ala Ser Phe Arg Arg
485 490 495

Ala Phe Val Asp Thr Phe Lys Gly Leu Pro Trp Arg Arg Gly Ala Gly
500 505 510

Ala Ser Gly Gly Val Gly Gly Ala Ala Gly Gly Gly Leu Ser Ala Ser
515 520 525

Gln Ala Gly Ala Gly Pro Gly Ala Tyr Ala Ser Ala Asn Thr Asn Ile
530 535 540

Ser Leu Asn Pro Gly Leu Ala Met Gly Met Gly Thr Trp Arg Ser Arg
545 550 555 560

Ser Arg His Glu Phe Leu Asn Ala Val Val Thr Thr Asn Ser Ala Ala
565 570 575

Ala Ala Val Asn Ser Pro Gln Leu
580

<210> 23

<211> 1452

<212> DNA

<213> D. melanogaster

<400> 23
atgtacgcct ctttgatgga cgttggccag acgttggcag ccaggctggc ggatagcgac 60
ggcaacgggg ccaatgacag cggactcctg gcaaccggac aaggtctgga gcaggagcag 120
gagggctctgg cactggatat gggccacaat gccagcggcg acggcggaat agtaccgtat 180
gtgcccgtgc tggaccgccc ggagacgtac attgtcaccc tgctgtacac gctcatcttc 240
attgtggag ttttggcaa cggcacgctg gtcacatct tctttcgcca ccgctccatg 300
cgcaacatac ccaacacata cattcttca ctggccctgg ctgatctgtt gtttatattg 360
gtgtgtgtac ctgtggccac gattgtctac acgcaggaaa gctggccctt tgagcggAAC 420
atgtccgca tcagcgagtt cttaaggac atatccatcg gggtgtccgt gtttacactg 480
accggccctt cggcgagcg gtactgcgcc attgtaaatc ccctacgcaa gttcagacc 540
aagccgctca ctgtcttac tgccgtgatg atctggatcc tggccatcct actggccatg 600

ccttcggttc ttttctccga catcaagtcc taccctgtgt tcacagccac cggttaacatg	660
accattgaag tggctcccc atttcgcgac ccggagtatg caaagttcat ggtggcggc	720
aaggcactgg tggactacct gttgccgctg tccatcattg gggcgctata catcatgatg	780
gccaagcggc tccatatgag cgcccgcaac atgcccggcg aacagcagag catgcagagc	840
cgcacccagg ctagggcccg actccatgtg ggcgcatgg tggtagcatt cgtggtgg	900
ttcttcatct gcttcttccc gtaccacgtg tttgagctgt ggtaccactt ctacccaacg	960
gctgaggagg acttcgatga gttctgaaac gtgctgcgca tccttcctaa actcgtgcgt	1020
caaccccggtg gcctctactg cgtgtccggg gtgttcggc agcactttaa tcgctaccc	1080
tgctgcatct ggcgtcaagcg gcagccgcac ctgcggcagc actcaacggc cactggaatg	1140
atggacaata ccagtgtgat gtccatgcgc cgctccacgt acgtgggtgg aaccgctggc	1200
aatctgcggg cctcgctgca ccggaacagc aatcacggag ttgggggagc tggaggtgga	1260
gtaggaggag gacttagggtc aggtcgtgtg ggcagcttc atcggcagga ctcgatgccc	1320
ctgcagcactg gaaatgccc cggaggtggc gccccgggg gatcctccgg acttggagcc	1380
ggcggggcggc cggcggcagt gaggaaaaag agctttataa atcgttacga aagtggcgta	1440
atgcgctact aa	1452

<210> 24

<211> 483

<212> PRT

<213> D. melanogaster

<400> 24

Met Tyr Ala Ser Leu Met Asp Val Gly Gln Thr Leu Ala Ala Arg Leu			
1	5	10	15
10	15		

Ala Asp Ser Asp Gly Asn Gly Ala Asn Asp Ser Gly Leu Leu Ala Thr			
20	25	30	
30			

Gly Gln Gly Leu Glu Gln Glu Gln Glu Gly Leu Ala Leu Asp Met Gly			
35	40	45	
45			

His Asn Ala Ser Ala Asp Gly Gly Ile Val Pro Tyr Val Pro Val Leu			
50	55	60	
60			

Asp Arg Pro Glu Thr Tyr Ile Val Thr Val Leu Tyr Thr Leu Ile Phe	
	Page 39

65

70

75

80

Ile Val Gly Val Leu Gly Asn Gly Thr Leu Val Ile Ile Phe Phe Arg
85 90 95

His Arg Ser Met Arg Asn Ile Pro Asn Thr Tyr Ile Leu Ser Leu Ala
100 105 110

Leu Ala Asp Leu Leu Val Ile Leu Val Cys Val Pro Val Ala Thr Ile
115 120 125

Val Tyr Thr Gln Glu Ser Trp Pro Phe Glu Arg Asn Met Cys Arg Ile
130 135 140

Ser Glu Phe Phe Lys Asp Ile Ser Ile Gly Val Ser Val Phe Thr Leu
145 150 155 160

Thr Ala Leu Ser Gly Glu Arg Tyr Cys Ala Ile Val Asn Pro Leu Arg
165 170 175

Lys Leu Gln Thr Lys Pro Leu Thr Val Phe Thr Ala Val Met Ile Trp
180 185 190

Ile Leu Ala Ile Leu Leu Gly Met Pro Ser Val Leu Phe Ser Asp Ile
195 200 205

Lys Ser Tyr Pro Val Phe Thr Ala Thr Gly Asn Met Thr Ile Glu Val
210 215 220

Cys Ser Pro Phe Arg Asp Pro Glu Tyr Ala Lys Phe Met Val Ala Gly
225 230 235 240

Lys Ala Leu Val Tyr Tyr Leu Leu Pro Leu Ser Ile Ile Gly Ala Leu
245 250 255

Tyr Ile Met Met Ala Lys Arg Leu His Met Ser Ala Arg Asn Met Pro
260 265 270

Gly Glu Gln Gln Ser Met Gln Ser Arg Thr Gln Ala Arg Ala Arg Leu
275 280 285

His Val Ala Arg Met Val Val Ala Phe Val Val Val Phe Phe Ile Cys
290 295 300

Phe Phe Pro Tyr His Val Phe Glu Leu Trp Tyr His Phe Tyr Pro Thr
Page 40

305

310

315

320

Ala Glu Glu Asp Phe Asp Glu Phe Trp Asn Val Leu Arg Ile Leu Pro
325 330 335

Lys Leu Val Arg Gln Pro Arg Gly Leu Tyr Cys Val Ser Gly Val Phe
340 345 350

Arg Gln His Phe Asn Arg Tyr Leu Cys Cys Ile Cys Val Lys Arg Gln
355 360 365

Pro His Leu Arg Gln His Ser Thr Ala Thr Gly Met Met Asp Asn Thr
370 375 380

Ser Val Met Ser Met Arg Arg Ser Thr Tyr Val Gly Gly Thr Ala Gly
385 390 395 400

Asn Leu Arg Ala Ser Leu His Arg Asn Ser Asn His Gly Val Gly Gly
405 410 415

Ala Gly Gly Val Gly Gly Val Gly Ser Gly Arg Val Gly Ser
420 425 430

Phe His Arg Gln Asp Ser Met Pro Leu Gln His Gly Asn Ala His Gly
435 440 445

Gly Gly Ala Gly Gly Ser Ser Gly Leu Gly Ala Gly Gly Arg Thr
450 455 460

Ala Ala Val Ser Glu Lys Ser Phe Ile Asn Arg Tyr Glu Ser Gly Val
465 470 475 480

Met Arg Tyr

<210> 25

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 25

Thr Asp Val Asp His Val Phe Leu Arg Phe
1 5 10

<210> 26

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 26

Asp Pro Lys Gln Asp Phe Met Arg Phe
1 5

<210> 27

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 27

Pro Asp Asn Phe Met Arg Phe
1 5

<210> 28

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 28

Thr Pro Ala Glu Asp Phe Met Arg Phe
1 5

<210> 29

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 29

Ser Leu Lys Gln Asp Phe Met His Phe
1 5

<210> 30

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 30

Ser Val Lys Gln Asp Phe Met His Phe
1 5

<210> 31

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 31

Ala Ala Met Asp Arg Tyr
1 5

<210> 32

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 32

Ser Val Gln Asp Asn Phe Met His Phe
1 5

<210> 33

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 33

Ala Arg Gly Pro Gln Leu Arg Leu Arg Phe
1 5 10

<210> 34

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 34

Gly Asp Gly Arg Leu Tyr Ala Phe Gly Leu
1 5 10

<210> 35

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 35

Asp Arg Leu Tyr Ser Phe Gly Leu
1 5

<210> 36

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 36

Ala Pro Ser Gly Ala Gln Arg Leu Tyr Gly Phe Gly Leu
1 5 10

<210> 37

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 37

Gly Gly Ser Leu Tyr Ser Phe Gly Leu
1 5

<210> 38

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 38

Phe Ile Arg Phe
1

<210> 39

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 39

Lys Asn Glu Phe Ile Arg Phe
1 5

<210> 40

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 40

Phe Met Arg Phe
1

<210> 41

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 41

Lys Ser Ala Phe Met Arg Phe
1 5

<210> 42

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 42

Lys Pro Asn Phe Leu Arg Phe
1 5

<210> 43

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 43

Phe Leu Arg Phe
1

<210> 44

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 44

Tyr Leu Arg Phe
1

<210> 45

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 45

Lys Pro Asn Phe Leu Arg Tyr
1 5

<210> 46

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 46

Thr Asn Arg Asn Phe Leu Arg Phe
1 5

<210> 47

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 47

Arg Asn Lys Phe Glu Phe Ile Arg Phe
1 5

<210> 48

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 48

Ala Gly Pro Arg Phe Ile Arg Phe
1 5

<210> 49

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 49

Gly Leu Gly Pro Arg Pro Leu Arg Phe
1 5

<210> 50

<211> 2

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 50

Ile Leu
1

<210> 51

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 51

Ala Gly Ala Lys Ile Phe Arg Phe
1 5

<210> 52

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 52

Ala Pro Lys Pro Lys Phe Ile Arg Phe
1 5

<210> 53

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 53

Lys Ser Ala Phe Val Leu Arg Phe
1 5

<210> 54

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 54

Thr Lys Phe Gln Asp Phe Leu Arg Phe
1 5

<210> 55

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 55

Ser Ala Glu Pro Phe Gly Thr Met Arg Phe
1 5 10

<210> 56

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 56

Ala Ser Glu Asp Ala Leu Phe Gly Thr Met Arg Phe
1 5 10

<210> 57

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 57

Ser Ala Asp Asp Ser Ala Pro Phe Gly Thr Met Arg Phe
1 5 10

<210> 58

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 58

Glu Asp Gly Asn Ala Pro Phe Gly Thr Met Arg Phe
1 5 10

<210> 59

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 59

Phe Leu Phe Gln Pro Gln Arg Phe
1 5

<210> 60

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 60

Ser Ala Asp Pro Asn Phe Leu Arg Phe
1 5

<210> 61

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 61

Ser Gln Pro Asn Phe Leu Arg Phe
1 5

<210> 62

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 62

Ala Ser Gly Asp Pro Asn Phe Leu Arg Phe
1 5 10

<210> 63

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 63

Ser Asp Pro Asn Phe Leu Arg Phe
1 5

<210> 64

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 64

Ala Ala Ala Asp Pro Asn Phe Leu Arg Phe
1. 5 10

<210> 65

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 65

Pro Asn Phe Leu Arg Phe
1 5

<210> 66

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 66

Lys Pro Phe Leu Arg Phe
1 5

<210> 67

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 67

Ala Gly Ser Asp Pro Asn Phe Leu Arg Phe
1 5 10

<210> 68

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 68

Lys Pro Asn Phe Leu Arg Tyr
1 5

<210> 69

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 69

Ser Pro Arg Glu Pro Ile Arg Phe
1 5

<210> 70

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 70

Leu Arg Gly Glu Pro Ile Arg Phe
1 5

<210> 71

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 71

Ser Pro Leu Gly Thr Met Arg Phe
1 5

<210> 72

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 72

Glu Ala Glu Glu Pro Leu Gly Thr Met Arg Phe
1 5 10

<210> 73

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 73

Ala Ser Glu Asp Ala Leu Phe Gly Thr Met Arg Phe
1 5 10

<210> 74

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 74

Glu Asp Gly Asn Ala Pro Phe Gly Thr Met Arg Phe
1 5 10

<210> 75

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 75

Ser Ala Glu Pro Phe Gly Thr Met Arg Phe
1 5 10

<210> 76

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 76

Ser Ala Asp Asp Ser Ala Pro Phe Gly Thr Met Arg Phe
1 5 10

<210> 77

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 77

Lys Pro Thr Phe Ile Arg Phe
1 5

<210> 78

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 78

Ala Ser Pro Ser Phe Ile Arg Phe
1 5

<210> 79

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 79

Gly Ala Lys Phe Ile Arg Phe
1 5

<210> 80

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 80

Ala Gly Ala Lys Phe Ile Arg Phe
1 5

<210> 81

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 81

Ala Pro Lys Pro Lys Phe Ile Arg Phe
1 5

<210> 82

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 82

Lys Ser Ala Tyr Met Arg Phe
1 5

<210> 83

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 83

Ser Pro Met Gln Arg Ser Ser Met Val Arg Phe
1 5 10

<210> 84

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 84

Ser Pro Met Glu Arg Ser Ala Met Val Arg Phe
1 5 10

<210> 85

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 85

Ser Pro Met Asp Arg Ser Lys Met Val Arg Phe
1 5 10

<210> 86

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 86

Lys Asn Glu Phe Ile Arg Phe
1 5

<210> 87

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 87

Lys Pro Ser Phe Val Arg Phe
1 5

<210> 88

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 88

Gln Pro Lys Ala Arg Ser Gly Tyr Ile Arg Phe
1 5 10

<210> 89

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 89

Ala Met Arg Asn Ala Leu Val Arg Phe
1 5

<210> 90

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 90

Ala Ser Gly Gly Met Arg Asn Ala Leu Val Arg Phe
1 5 10

<210> 91

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 91

Asn Gly Ala Pro Gln Pro Phe Val Arg Phe
1 5 10

<210> 92

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 92

Arg Asn Lys Phe Glu Phe Ile Arg Phe
1 5

<210> 93

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 93

Ser Asp Arg Pro Thr Arg Ala Met Asp Ser Pro Ile Arg Phe
1 5 10

<210> 94

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

400> 94

la Ala Asp Gly Ala Pro Leu Ile Arg Phe
5 10

210> 95

211> 10

212> PRT

213> Artificial Sequence

220>

223> Novel Sequence

400> 95

la Pro Glu Ala Ser Pro Phe Ile Arg Phe
5 10

210> 96

211> 10

212> PRT

213> Artificial Sequence

220>

223> Novel Sequence

400> 96

la Ser Pro Ser Ala Pro Leu Ile Arg Phe
5 10

210> 97

211> 10

212> PRT

213> Artificial Sequence

220>

223> Novel Sequence

<400> 100

Ser Leu Asp Tyr Arg Phe
1 5

<210> 101

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 101

Glu Ile Val Phe His Gln Ile Ser Pro Ile Phe Phe Arg Phe
1 5 10

<210> 102

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 102

Gly Gly Pro Gln Gly Pro Leu Arg Phe
1 5

<210> 103

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 103

Gly Pro Ser Gly Pro Leu Arg Phe
1 5

<210> 104

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 104

Ala Gln Thr Phe Val Arg Phe
1 5

<210> 105

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 105

Gly Gln Thr Phe Val Arg Phe
1 5

<210> 106

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 106

Lys Ser Ala Phe Val Arg Phe
1 5

<210> 107

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 107

Lys Ser Gln Tyr Ile Arg Phe
1 5

<210> 108

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 108

Asp Val Pro Gly Val Leu Arg Phe
1 5

<210> 109

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 109

Lys Ser Val Pro Gly Val Leu Arg Phe
1 5

<210> 110

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 110

Ser Glu Val Pro Gly Val Leu Arg Phe
1 5

<210> 111

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 111

Ser Val Pro Gly Val Leu Arg Phe
1 5

<210> 112

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 112

Asp Phe Asp Gly Ala Met Pro Gly Val Leu Arg Phe
1 5 10

<210> 113

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 113

Glu Ile Pro Gly Val Leu Arg Phe
1 5

<210> 114

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 114

Trp Ala Asn Gln Val Arg Phe
1 5

<210> 115

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 115

Ala Ser Trp Ala Ser Ser Val Arg Phe
1 5

<210> 116

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 116

Ala Met Met Arg Phe
1 5

<210> 117

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 117

Gly Leu Gly Pro Arg Pro Leu Arg Phe
1 5

<210> 118

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 118

Ser Pro Ser Ala Lys Trp Met Arg Phe
1 5

<210> 119

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 119

Thr Lys Phe Gln Asp Phe Leu Arg Phe
1 5

<210> 120

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 120

Glu Asp Arg Asp Tyr Arg Pro Leu Gln Phe
1 5 10

<210> 121

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 121

Phe Ile Arg Phe
1

<210> 122

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 122

Ala Val Pro Gly Val Leu Arg Phe
1 5

<210> 123

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 123

Gly Asp Val Pro Gly Val Leu Arg Phe
1 5

<210> 124

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 124

Ser Asp Ile Gly Ile Ser Glu Pro Asn Phe Leu Arg Phe
1 5 10

<210> 125

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 125

Ser Gly Lys Pro Thr Phe Ile Arg Phe
1 5

<210> 126

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 126

Ala Glu Gly Leu Ser Ser Pro Leu Ile Arg Phe
1 5 10

<210> 127

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 127

Phe Asp Arg Asp Phe Met Arg Phe
1 5

<210> 128

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 128

Ala Gly Pro Arg Phe Ile Arg Phe
1 5

<210> 129

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 129

Gly Met Pro Gly Val Leu Arg Phe
1 5

<210> 130

<211> 2

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 130

Ile Leu
1

<210> 131

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 131

Leu Gln Pro Asn Phe Leu Arg Phe
1 5

<210> 132

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 132

Lys Pro Asn Phe Ile Arg Phe
1 5

<210> 133

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 133

Phe Met Arg Phe
1

<210> 134

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 134

Phe Leu Arg Phe
1

<210> 135

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 135

Tyr Ile Arg Phe
1

<210> 136

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 136

Gly Asn Ser Phe Leu Arg Phe
1 5

<210> 137

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 137

Asp Pro Ser Phe Leu Arg Phe
1 5

<210> 138

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 138

Gln Asp Phe Met Arg Phe
1 5

<210> 139

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 139

Lys Pro Asn Gln Asp Phe Met Arg Phe
1 5

<210> 140

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 140

Thr Asp Val Asp His Val Phe Leu Arg Phe
1 5 10

<210> 141

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 141

Ala Ala Met Asp Arg Tyr
1 5

<210> 142

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 142

Ser Pro Lys Gln Asp Phe Met Arg Phe
1 5

<210> 143

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 143

Pro Asp Asn Phe Met Arg Phe
1 5

<210> 144

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 144

Asp Pro Lys Gln Asp Phe Met Arg Phe
1 5

<210> 145

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 145

Thr Pro Ala Glu Asp Phe Met Arg Phe
1 5

<210> 146

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 146

Ser Asp Asn Phe Met Arg Phe
1 5

<210> 147

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 147

Tyr Leu Arg Phe
1

<210> 148

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 148

Ser Asp Arg Asn Phe Leu Arg Phe
1 5

<210> 149

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 149

Thr Asn Arg Asn Phe Leu Arg Phe
1 5

<210> 150

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 150

Pro Asp Val Asp His Val Phe Leu Arg Phe
1 5 10

<210> 151

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 151

Gln Asp Val Asp His Val Phe Leu Arg Phe
1 5 10

<210> 152

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 152

Phe Leu Phe Gln Pro Gln Arg Phe
1 5

<210> 153

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 153

Ala Arg Gly Pro Gln Leu Arg Leu Arg Phe
1 5 10

<210> 154

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 154

Phe Asp Asp Tyr Gly His Leu Arg Phe
1 5

<210> 155

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 155

Phe Asp Asp Tyr Gly His Leu Arg Phe
1 5

<210> 156

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 156

Met Asp Ser Asn Phe Ile Arg Phe
1 5

<210> 157

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 157

Phe Asp Asp Tyr Gly His Leu Arg Phe
1 5

<210> 158

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 158

Phe Asp Asp Tyr Gly His Leu Arg Phe
1 5

<210> 159

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 159

Phe Asp Asp Tyr Gly His Met Arg Phe
1 5

<210> 160

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

~ <400> 160

Gly Gly Asp Asp Gln Phe Asp Asp Tyr Gly His Met Arg Phe
1 5 10

<210> 161

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 161

Ser Arg Pro Tyr Ser Phe Gly Leu
1 5

<210> 162

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 162

Asp Tyr Gly His Met Arg Phe
1 5

<210> 163

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 163

Ala Pro Arg Thr Pro Gly Gly Arg Arg
1 5

<210> 164

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 164

Val Glu Arg Tyr Ala Phe Gly Leu
1 5

<210> 165

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 165

Leu Pro Val Tyr Asn Phe Gly Leu
1 5

<210> 166

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 166

Thr Thr Arg Pro Gln Pro Phe Asn Phe Gly Leu
1 5 10

<210> 167

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 167

Glu Asp Val Asp His Val Phe Leu Arg Phe
1 5 10

<210> 168

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 168

Gly Asn Ser Phe Leu Arg Phe
1 5

<210> 169

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 169

Ala Pro Thr Ser Ser Phe Ile Gly Met Arg
1 5 10

<210> 170
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 170

Ala Pro Leu Ala Phe Tyr Gly Met Arg
1 5

<210> 171
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 171

Ala Pro Leu Ala Phe Tyr Gly Leu Arg
1 5

<210> 172
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 172

Ala Pro Thr Gly Phe Thr Gly Met Arg
1 5

<210> 173
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 173

Ala Pro Val Asn Ser Phe Val Gly Met Arg
1 5 10

<210> 174
<211> 9
<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 174

Ala Pro Asn Gly Phe Leu Gly Met Arg
1 5

<210> 175

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 175

Asp Pro Ala Phe Asn Ser Trp Gly
1 5

<210> 176

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 176

Gly Ser Gly Phe Ser Ser Trp Gly
1 5

<210> 177

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<220>

<221> MOD_RES

<222> (1)..(1)

<223> Residue at position 1 is pGlu.

<400> 177

Xaa Ser Ser Phe His Ser Trp Gly
1 5

<210> 178

<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 178

Gly Ala Ser Phe Tyr Ser Trp Gly
1 5

<210> 179
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 179

Asn Pro Phe His Ser Trp Gly
1 5

<210> 180
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 180

Pro Ser Phe His Ser Trp Ser
1 5

<210> 181
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 181

Asn Ser Val Val Leu Gly Lys Lys Gln Arg Phe His Ser Trp Gly
1 5 10 15

<210> 182
<211> 15
<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<220>

<221> MOD_RES

<222> (1)..(1)

<223> Xaa is pGlu.

<400> 182

Xaa Val Arg Phe Arg Gln Cys Tyr Phe Asn Pro Ile Ser Cys Phe
1 5 10 15

<210> 183

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 183

Gln Arg Phe His Ser Trp Gly
1 5

<210> 184

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<220>

<221> MOD_RES

<222> (1)..(1)

<223> Xaa is pGlu

<221> DISULFID

<222> (7)..(14)

<400> 184

Xaa Val Arg Phe Gln Cys Tyr Phe Asn Pro Ile Ser Cys Phe
1 5 10

<210> 185

<211> 15

<212> PRT

<213> Artificial Sequence

<220>